GenCore version 5.1.3 copyright (c) 1993 - 2003 Compugen Ltd.

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(without alignments)
122.402 Million cell updates/sec
                                    January 16, 2003, 16:58:02 ; Search time 661.571 Seconds
nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eukaryola: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta; eudicotyledons: core endicots: Rosidae: eurosids II; Brassicales; Brassicaceae: Arabidopsis. 1 (bases 1 to 102) Rounsley,S.D., Suh,E.J., Wible,C., Golden,K., Shatsman,S., Choi,P., AQUI0934 1058 29-MAY-1998 F23C7TRC GF Arabidopsis thaliana genomic clone F23C7, DNA AQ010934 AQ010934.1 GI:3165707 Arabidopsis thaliana thale cress. sequence RESULT 1 AQ010934/c DEFINITION ACCESSION VERSION ORGANISM REFERENCE AUTHORS KEYWORDS SOCO?

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Percent Similarity:
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Produced by Thomas Altmann"
Yu, K., Akinictoye, B., Shen, K., Goomasekaram, S., Militscher, J., Adams, M.D. and Venter, J.C.
Adams, M.D. and Venter, J.C.
A BAC End Sequence Dalabase for Identifying Minimal Overlaps in
Arabidopsis Genomic Sequencing, Update 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
This clone is available royally free through LLML . contact the TMAGE Consortium (infodimate.llnl.qov) for further information. Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MO 63108
                                                                                                                                                   9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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                                                                                                                                       The Institute for Genomic Research
                                                                                                  Contact: Steve Rounsley
Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                                                                             /strain-"Columbia"
/db_xret-"taxon:3702"
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/sex-"hermaphrodite"
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                                                                                                                                                                                                        Email: rounsleydtigr.ord
Seq primer: M13 Reverse
Class: BAC ends
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/inche-"Vector: pseudil: site_1: sall; Site_2: Not1: RNA was prepared from a pool of 6 anotymous Wilms' tumor KNAS. RNA was prepared by acid-phenol, followed by one round of oliqo d'selection. CDNA library preparation was with the BRL/Lie Tech. Superscript Plasmid system. An oliqo-d's Not1 primer for list strand synthesis generated gradecore(t)n at the 3' end off the clones. A 5' Sall adaptor was used with sequence 5'-qtoqacoreaque(cq-4') Resulting cDNAs were size solected (average size 2 kb), Not1 digested, and lighted into Not1/Sall-cut pSPORII. Library was constructed and lighted and lighted and solected (assignment psporii).
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Stam, M., Longarte, S., Mahmoud, M., Mesuru, E., Pederseu, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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2M0101508F Mouse 15kb plasmid UUGCIM library Mus museulus genomie
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Seg primer: -40mi3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualitiers
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/db_xrgt="taxon:9606"
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University of Utah Genome Center
University of Utah
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Insert Length: 10000 - Std Erro
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Fax: 801 585 7177
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КСZ-ETÚČLA-ZÝG4GO-GLZ-CGZ ETGŰLM Homo sapiens CNNA, mPNA sequence.
AW946335
                                                                                                                                                                                                                                                                                                       was hydrodynamically sheared by repeated passage through a 0.005 inch crifice at constant velocity. The sheared DNA was bluit and repaired with T4 DNA polymerase and T4 polymerated to the bluit ends in high molar excess. The adaptored DNA was puritied and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. "

15 c 34 q 31 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwind (gild732114) galgar12902.1), a copy-number inductible derivative of plasmid P1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota: Metacoa; Chordata, Craniata, Veriebrata, Euleleostomi,
Mammalia; Butheria, Primates; Catarthini; Hominidae; Homo.
1 (bases 1 to 115)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/) The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Paia, G.S., Simpson, D. H. Brunstein, A., deoliveira, P.S., Rucher, P., Tongeneel, C.V., O'Hare, M.J., Soares, F., Rrentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                            /note-"Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Lakoratory Mouse DNA Pescurre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                      /sex-"Male"
/lab_host "E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                           /clone_lib-"Mouse 10kb plasmid UUGC1M library"
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Mismatches:
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/organism-"Mus musculus"
                                                  /db_xref="taxon-10090"
/close="mmgc2M0101g08"
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                       /strain-"C57HL/6.1"
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Fax: +55-11-2707001
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/dev_stage="Addit"
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This sequence was derived from the FAPESP/LICR Human Caneer Genome Project. This entry can be seen in the following URL Chip://www.lidwig.org.br/scripts/gethtml2.pl?tl-st2-pr2-pr018 290 869 primer: pue 18 forward
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1M0556707F Mouse 10kb plasmid UEGCIM library Mus musculus genomic
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1 (bases 1 to 127)
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Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostumi;
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/db_xret="taxon:9606"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                     High quality sequence start: 9
High quality sequence stop: 115.
i.ocation/Qualifiers
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Fax: 801 585 7177
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us-09-856-070-18.rst

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/mode Vorgan: Fancreas; Vector: phluescript sk(-); site_1:
Not; Site_2: Xhol; cNNA made by oligo-d1 priming.
Size:selected on agarose gel. Average insert size:tkb, 5;
Xhol site was destroyed after directional cloning.
Muplified once. Contact information: Hiroshi Inoue, MD,
MH-1d-ism Fiv. (Alan Fermittiak). Rashington Holiensity
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MD 5310, E mail: hinoue*imgate.wustl.edu. Tel:
a 37 g 38 t
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Nagai, M.A., da Silva, W. Jr., Zaqo, M.A., Bordin, S., Costa, F.F.,
Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Gollvelfan, P.S., Bucher, P., Jongeneel, C.V., O'Hare
.M.J., Soares, F., Brentani, K.R., Reis, L.F., de Souza, S.J., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson*ludwig.org.br
This sequence was derived from the PAPESP/GICE Homen Cancer Genome
Project. This entry can be seen in the following URL
Chilip...www.lodwig.org.br/solipts/getHimiz.plc11 kdlatz kdl-sT0278-
     Washington University Genome Sequencing Center For information on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509 010, Sao Paulo SP,
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PCL-ST0278 200909 110-d11_2 ST0278 Homp sapiens CDNA, mkNA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-4496 (2000)
                               obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                      /organism-"Homo sapiens"
//db.xref="taxon:9606"
//clouc_lib-HR85 islet"
/Lissue_lype-"Puritied pancreatic islet"
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                                                       (hinoucalm.wustl.cdu)
Trace considered overall poor quality
Seg primer: 40MP from Gibco
High quality sequence stop: 1.
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Laboratory of Cancer Genetics
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                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnates/). The unha was hydro-ynamically sheared by repeated jassage through a was hydro-ynamical constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerace rounder kinase. Adaptor oligosucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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(bases 1 to 130)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Icmishka,I., Sordrew,M., Papc,D., Wylie,I., Martin,J., Histain,S.,
Hillor,L., Marra,M., Papc,D., Wylie,I., Martin,J., Histain,A.,
Schmitt,A., Theising,M., Ritter,E., Ronko,I., Henstain,A.,
M., Gibbons,M., McCann,R., Cole,R., Tsaqareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mukaryota: Metazoa; Chordata; Cramiata; Vertebrata, Eulteleostumi;
                                                                                                                                                               /note-"Vector: PWD42nv; Purified genomic DNA from M
musculus C578L/6.1 (male) was obtained from the Jackson
                                                                                                                                     /lab_host-"E. Coli strain XL10-Gold, Tl-resistant, F-"
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 Library was constracted by Dr. Hiroshi Incue DNA sequencing \mathbb{L}_T.
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                                                                              /clone_lib="Mouse 10kb plasmid UUGClM library"
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                          /db_xret-"taxon:10090"
                                                 /clone-"UUGC1M0556J07"
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Unpublished (2000)
Other_ESTS: ig68b04.x1
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/strain-"C57BL/6J"
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COMMENT

/db\_xret "taxon:9606"

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Percent Similarity:
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/db_xref--laxon.9606*
/db_xref--laxon.9608*
/dcone_lib--sru278*
/dcv_srager-Adult*
/dcv_srager-Adult*
/rote--forgar: stemath, Vector. pucl8, Site_1: Smal,
Site_2: Smai, A mini library was made by cloning products
derived from ORESIES PCR (U.S. Letters Patent application
No. 196.716 - Undwig Insiliute for Cancer Research)
profiles into the pig 18 vector Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
14 a 25 c 35 g 26 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 bp mRNA linear EST UZ-FEB-1997 z163cil.rl Soares_letal_livet_spleed_lNFLS.51 Homo sapiens FinA Clone IMAGE:416755 5' similar to SWERLER_MOSE PZWES6 BFAIN PROTEIN W86729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Educator, Chordata, Ctaniata, Vertebrata, Educioustomi, Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

(base. 1 to 136)
Hillier. L. Lennon. G. Becker. M., Bonaldo, M. F., Chiapelli, R., Chissoe, S., Dierrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, Schellenberg, K., Scarcs, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmarn, P., Waterstön, R., Wilson, R. and Marra, M. Generalion and analysis of 1280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL,; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 957 - 81d Error: 0-00
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Junselvative.
Mismatches:
290000-110-411_281+...oco.-04-20814-1)
Seq primer: puc 18 forward
High quality sequence stop: 130.
Location/Qualifiers
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/db_xret="GDB:1325226"
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JOURNAL
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double-stranded cDNA was ligated to Eco KI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT713 vector. Library and Eco RI sites of the modified pT713 vector. Library constructed by Nento Sources and M.Patima Honaldo."
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Enkaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:
Mammalia: Eutheria: Filmates: Catarihini, Hominidae: Homo.
1 (bases 1 to 137)
Dias Neto,E., Garcia Correa.R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPFSP/LICK Human Cancer Genome Project. This entry can be seen in the following URL (bitp://www.lidwig.org.br/scripts/getbtml2_pl2t1.xt2-wPl-UM0004-180
                                                                          00774394 EST 20-SEP-2000 MET-10000 Incor EST 20-SEP-2000 MPT-1000009-100500-014-bio UMBOOP Homo Sapiens CDNA, MENA sequence.
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                                                                                                                                                                                                                        1st strand cDNA was primed
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Ludwig Institute for Cancer Research
Bua Prof. Antosio Prudonte 109, 4 andar, 01509-010, Sac Paulo SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgan sequencing of the human transcriptome with GRF expressed
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/sex-"male"
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High quality sequence stop: 137.
Location/Qualifiers
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Seq primer: puc 18 forward
/clone-"IMAGE:416756"
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Fax: +55-11-2707001
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                                                                                   /note-*Organ: uterus; Vector: pucl8; Site_1: Smal; Site_2: Smal; A min-library was made by cloning products derived From ORESTES DER (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research; profiles finto the pucl 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH811366 138 bp DNA linear CSS 02-MAY-2002 SALK_058499 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana quomic clone SALK_058499, DNA sequence.
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/clone-"SALK_058459"
/clone-"SALK_058459"
/clone-lb "Astabidopsis thaliana TDNA insertion lines"
/note-"PCP was performed on Arabidopsis thaliana lines
cach of which contains one or more IDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the qenomic sequence at
the site of insertion. Details of the protocols used can
be found at http://sianal.salk.edu/idma_protocols.html"
A7 c 25 g 36 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryola, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, cole eudicots;
Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is simple pass sequence recovered from the left border of TONA. This sequence lies within an annotated exon of AtAq1774n
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Unpublished (2001)
Contact: Joseph R Erker
Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 658 6579
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/strain-"Columbia 0"
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Mismatches
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/organism "Homo sapiens"
/db_vrof="tayon:9606"
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                                        /clone_lib-"UM0009"
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1. .138
                                                             /dev_staye-"Adult"
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Email: asimpson-fludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome-
Project This entry can be seen in the following URL
(http://www.nodwig.crj.br/scripts/gcriftind2.pizti-st2-RC2-E10019-080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xvio.memborsapicus./db_xvio.memborsapicus./db_xvio.memborsapicus./db_xvio.memborsapicus./db_xvio.memborsapicus./db_xvio.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.memborsapicus./doct.me
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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EC2-ETU019-080500-012 fl2 LT0019 Homo Sapiens CDNA, mKNA sequence.
AW946443
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 139)
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Labotatory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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High quality sequence start: 13
High quality sequence stop: 139.
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Fax: +55-11-2707001
                                                                                                      100.008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the mouse BAC library PPC1-24. For HAC library availability, please contact Pictor de Jong (ppc)ongemaniche.org). Chones may be purchased from HACPAC Resources (http://www.rigr.org/fdb/papac/orderingframe htm). BAC end page: http://www.rigr.org/fdb/pac_ends/mouse/foot_end_infro.html Seq primer: 77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1: Site_1: BamH1: Site_2: BamH1:
RPCT-24 Mouse BAC Library produced by Pictor de Jong. The
Library was cloued in the pTARBAC1 cioning vector at the
HamH1 sites using Mbol partially digested male C57H1/61
DNA."
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Eukaryota, McLuson; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria; Rodentia; Sciuroguathi; Muzidae; Muzinae; Mus
1 (bases 1 to 143)
Zhao,S., Nlerman,R., Malek,J., Shatsman,S., Akinret,R., Levins,M.,
Frseqayo,G., Geet,K., Krol,M., Shvartsbeyn,A., Gebreyeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse MAC End Sequences from Library RPC1-24
Onpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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/clone-"RPC1-24-333H1"
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                                                      US-09-856-070-18 (1-5) x AW946443 (1-139)
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                                                                                                                                                                                                                                                                                        BH101135.1 GI:14925696
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17n 60%
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60 AAGGAGGAGCTGATG 74

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HR063341 FIXEN IUll-length enriched, in vitro lertilized eggs Musmusculus CDNA clone 7420484Pl3 3', mRNA sequence.
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Exaryolus, Mctacoa, Chordata, Craniata, Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 151)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishik, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Ilawa, M., Radota, K., Ragawa, I., Rai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Rodo, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Shibata, K., Shibata
BJ008375 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA119C09 5',
                                                                                                                                                                                                     Eckarysta, Metamoa, Chordata, Cramiata, Vertebrata, Esteleostomi, Astinopersygii, Neopersydi, Teleostoi, Mateleostei, Neoteleostei, Astinopersygii, Percomorpha, Atherinomorpha; Acanthopersygii, Percomorpha; Atherinomorpha; Belonitormes; Adrianichthyidae, Oryziinae; Cryzias.
                                                                                                                                                                                                                                                                                                         1 (bases 1 to 149)
Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
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0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1111 Yara, Mishima, Shizuoka 411-8540, Japan
101: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Contact: ladasu Shin-i
Pentar For Gepetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryzias latipes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tshin!@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:8090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-856-070-18 (1-5) x BJ008375 (1-149)
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                                                                                                 BJ008175 1 GI-17368489
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BJ008375
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Hest Local Similarity:
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EST 14-MAR-2002

Linear

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JOHNAL.

TITLE COMMENT

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1933905.y2 Molton Human islets FIZI Homo sapiens clone from 2002. IMAGE:5640152-5' similar to SW:CBPH_MOUSE 000493 CARHOXYDEPTIDASE H
PRECURSOR ;, mRNA sequence.
                                                                                                                                 HKNA
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                                                                                                                         151 bp
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Location/Qualifiers
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                                                                                                                                                                                                                                           BG141368.1 GI:12644762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.00
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       66 AAGGAGGAGCTGAIG 52
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BG141368
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.Y., Shiqemoto,Y., Shinaqawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Taqawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                Bmail: genome-resegsc.riken.ao.jp,
URL:http://denome-gsc.riken.ao.jp,
Garninci.P. Nishiyama.Y., Westover.A. Itoh.M., Nagaoka.S., Sasaki.N., Okazaki.Y.
N., Okazaki.Y. Murama*su.M. and Hayashiraki.Y.
Thermostablilization and thermoard:Sustion of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520 524 (1998)
Ifoh.M., Kilsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci.P., Shibata,Y., Owawa,Y., Muramaisu,M., Okaraki.Y., and Hayashiraki.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute.
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchito-cho, Tsurami-ku, Yokohama, Kanagawa 230 0045, Japan 101: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Pescarch Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKNE. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. Ist strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Automated filtration-based high-throughput plasmid preparation system common was 9 (5), 448-470 (1994) (Carninci, P. and Hayashizaki, Y. High-efficiency Iull-length cDNA cloning, Methods Enzymol. 303, High-efficiency Iull-length cDNA cloning, Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our meb site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib-"RIKEN full-length enriched, in vitro
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Mismatches:
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/clone-"7420484813"
                                                                                                                                             Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Source

FEATURES

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Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates: Catarrhini: Hominidae; Homo.

(bases 1 to 1 deases 1 to 1 dease, Clifton, S., Hillier, L., Marta, M., Pape, D., Mciton, D., Mcadows, A., Clifton, S., Hillier, L., Marta, M., Pape, D., Wylie, T., Martin, J., Histain, A., Schmitt, A., Theisinq, H., Ritter, E., Tangareishvill, R., Cardenas, M., Gibbons, M., McKann, R., Cole, R., Tangareishvill, R., Williams, T., Jackson, Y. and Bowers, Y. Washgillarvard Pancreas EST Project
                                                                                                                                                                                                                                                                                                                                                                                      Endocrine Pańcreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biclogy, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frace considered overall poor quality This sequence now available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /hote-"Organ: Pancreas; Vector: p2Ero-2; Site_1: Not 1; Site_2: Xho 1; Labrary constructed using SuperScript Plasmid Library kit (Lite Technologies), cDNA made hy oligo dT priming. Xho i site destroyed during cloning. Size: selected by column fractionation; average insert size 1:59 kb. primary library, unamplified."
                                                                                                                                                                                                                                                                                                                                                      Contact, Douglas Melton, Klaus H. Kaestner, & Hiroshi Inone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from the IMAGE consortium, for clone orders contact:
info@image.llnl.gov
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref "taxon:9500"
/clone-"iMAGE:5640152"
/clone-lib-"Melton Human Islets HIZ1"
/sex-"Both"
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HASE COUNT

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